

SEQUENCE LISTING

<110> University of Rochester

Chang, Chawnshang

<120> Non-androgen Dependent Roles for
Androgen Receptor and Non-androgen Related Inhibitors of
Androgen Receptor

<130> 21108.0037P1

<140> Unassigned

<141> 2004-12-13

<150> 60/529,011

<151> 2003-12-12

<160> 23

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 1

```

Met Ala Ala Val Glu Leu Glu Trp Ile Pro Glu Thr Leu Tyr Asn Thr
 1           5           10           15
Ala Ile Ser Ala Val Val Asp Asn Tyr Ile Arg Ser Arg Arg Asp Ile
          20           25           30
Arg Ser Leu Pro Glu Asn Ile Gln Phe Asp Val Tyr Tyr Lys Leu Tyr
      35           40           45
Gln Gln Gly Arg Leu Cys Gln Leu Gly Ser Glu Phe Cys Glu Leu Glu
 50           55           60
Val Phe Ala Lys Val Leu Arg Ala Leu Asp Lys Arg His Leu Leu His
 65           70           75           80
His Cys Phe Gln Ala Leu Met Asp His Gly Val Lys Val Ala Ser Val
          85           90           95
Leu Ala Tyr Ser Phe Ser Arg Arg Cys Ser Tyr Ile Ala Glu Ser Asp
      100          105          110
Ala Ala Val Lys Glu Lys Ala Ile Gln Val Gly Phe Val Leu Gly Gly
      115          120          125
Phe Leu Ser Asp Ala Gly Trp Tyr Ser Asp Ala Glu Lys Val Phe Leu
      130          135          140
Ser Cys Leu Gln Leu Cys Thr Leu His Asp Glu Met Leu His Trp Phe
      145          150          155          160
Arg Ala Val Glu Cys Cys Val Arg Leu Leu His Val Arg Asn Gly Asn
          165          170          175
Cys Lys Tyr His Leu Gly Glu Glu Thr Phe Lys Leu Ala Gln Thr Tyr
          180          185          190
Met Asp Lys Leu Ser Lys His Gly Gln Gln Ala Asn Lys Ala Ala Leu
          195          200          205
Tyr Gly Glu Leu Cys Ala Leu Leu Phe Ala Lys Ser His Tyr Asp Glu
      210          215          220

```

Ala Tyr Lys Trp Cys Ile Glu Ala Met Lys Glu Ile Thr Ala Gly Leu
 225 230 235 240
 Pro Val Lys Val Val Val Asp Val Leu Arg Gln Ala Ser Lys Ala Cys
 245 250 255
 Val Val Lys Arg Glu Phe Lys Lys Ala Glu Gln Leu Ile Lys His Ala
 260 265 270
 Val Tyr Leu Ala Arg Asp His Phe Gly Ser Lys His Pro Lys Tyr Ser
 275 280 285
 Asp Thr Leu Leu Asp Tyr Gly Phe Tyr Leu Leu Asn Val Asp Asn Ile
 290 295 300
 Cys Gln Ser Val Ala Ile Tyr Gln Ala Ala Leu Asp Ile Arg Gln Ser
 305 310 315 320
 Val Phe Gly Gly Lys Asn Ile His Val Ala Thr Ala His Glu Asp Leu
 325 330 335
 Ala Tyr Ser Ser Tyr Val His Gln Tyr Ser Ser Gly Lys Phe Asp Asn
 340 345 350
 Ala Leu Phe His Ala Glu Arg Ala Ile Gly Ile Ile Thr His Ile Leu
 355 360 365
 Pro Glu Asp His Leu Leu Leu Ala Ser Ser Lys Arg Val Lys Ala Leu
 370 375 380
 Ile Leu Glu Glu Ile Ala Ile Asp Cys His Asn Lys Glu Thr Glu Gln
 385 390 395 400
 Arg Leu Leu Gln Glu Ala His Asp Leu His Leu Ser Ser Leu Gln Leu
 405 410 415
 Ala Lys Lys Ala Phe Gly Glu Phe Asn Val Gln Thr Ala Lys His Tyr
 420 425 430
 Gly Asn Leu Gly Arg Leu Tyr Gln Ser Met Arg Lys Phe Lys Glu Ala
 435 440 445
 Glu Glu Met His Ile Lys Ala Ile Gln Ile Lys Glu Gln Leu Leu Gly
 450 455 460
 Gln Glu Asp Tyr Glu Val Ala Leu Ser Val Gly His Leu Ala Ser Leu
 465 470 475 480
 Tyr Asn Tyr Asp Met Asn Gln Tyr Glu Asn Ala Glu Lys Leu Tyr Leu
 485 490 495
 Arg Ser Ile Ala Ile Gly Lys Lys Leu Phe Gly Glu Gly Tyr Ser Gly
 500 505 510
 Leu Glu Tyr Asp Tyr Arg Gly Leu Ile Lys Leu Tyr Asn Ser Ile Gly
 515 520 525
 Asn Tyr Glu Lys Val Phe Glu Tyr His Asn Val Leu Ser Asn Trp Asn
 530 535 540
 Arg Leu Arg Asp Arg Gln Tyr Ser Val Thr Asp Ala Leu Glu Asp Val
 545 550 555 560
 Ser Thr Ser Pro Gln Ser Thr Glu Glu Val Val Gln Ser Phe Leu Ile
 565 570 575
 Ser Gln Asn Val Glu Gly Pro Ser Cys
 580 585

<210> 2

<211> 1758

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 2

atggcgggccg	tggaactaga	gtggatccca	gagactctct	ataacaccgc	catctccgct	60
gtcgtggaca	actacatccg	ctcccgccga	gacatccgct	ccttgcccga	gaacatccag	120
tttgatgttt	actacaagct	ttaccaacag	ggacgcttat	gtcaactggg	cagtgaattt	180
tgtgaattgg	aagtttttgc	taaagtactg	agagcttttg	ataaaagaca	tttgcttcat	240

cattgttttc	aggccttcat	ggatcatggt	gttaaagttg	cttcagtctt	ggcctactca	300
ttcagtaggc	ggtgctctta	tatagcagaa	tcagatgctg	cagtaaagga	aaaagccatt	360
caggttggct	ttgttttagg	tggctttctt	tcagatgcag	gctggtagag	tgatgctgag	420
aaagtttttc	tgtcctgcct	tcagttgtgt	actctacacg	atgagatgct	tcattgggtt	480
cgtgcagtag	aatgttgtgt	gaggttgctt	catgtgcgaa	atggaaactg	caaatatcat	540
ttgggtgaag	aaacatttaa	attagctcag	acatatatgg	ataaaactatc	aaaacatggc	600
cagcaagcaa	ataaagctgc	actctatgga	gaactgtgtg	cactcctatt	tgcaaaaagt	660
cactatgatg	aggcatacaa	atggtgcatc	gaggcaatga	aagaaattac	agcaggctta	720
ccagtgaag	ttgtgggtgga	tgtcttaaga	caagcttcta	aggcttgtgt	agtaaaacgt	780
gaatttaaga	aggcagaaca	gttaattaaa	catgcagtgt	atttggcacg	ggatcatttt	840
ggatccaaac	acccaaaata	ttctgataca	ctgctagatt	atgggttcta	cttactcaat	900
gtagataata	tctgtcagtc	tgttgcaatt	tatcaggcag	cccttgacat	tagacagtca	960
gtgtttgggt	gcaaaaatat	ccacgtagca	acagctcatg	aagatttggc	ctactcttct	1020
tatgtccacc	agtatagctc	tgggaaattt	gacaatgcac	tatttcatgc	agaaagagct	1080
attggtatca	ttaccacat	cctacctgaa	gatcatcttc	ttttggcttc	ttcaaagagg	1140
gtgaaagcac	ttattttaga	ggagattgca	attgattgtc	ataataagga	aactgaacag	1200
aggctgcttc	aagaagctca	tgatttgcac	ctgtcttcac	tccaactagc	taaaaaagct	1260
tttggggaat	ttaatgtaca	gactgcaaaa	cactatggaa	acotttgaag	actttatcag	1320
tcaatgagaa	aatttaagga	agctgaagaa	atgcacatca	aagcaattca	gattaaagaa	1380
caacttcttg	gtcaagaaga	ttatgaagta	gccctttcag	tgggacatct	ggcttcttta	1440
tataattatg	acatgaatca	gtatgaaaat	actgagaaac	tttatttgcg	atctatagca	1500
attgggaaga	aacttttttg	tgagggtctac	agtggactag	aatatgatta	tcgagggtctc	1560
attaaacttt	acaactccat	tggaaattac	gagaaagtgt	ttgaatatca	caatgttctg	1620
tctaactgga	accggttgcg	agatcggcaa	tattcagtga	cagatgctct	tgaagatgtc	1680
agcaccagcc	cccagtccac	tgaagaagtg	gtgcagtcct	tcctgatttc	tcagaatgtc	1740
gagggaccga	gctgctga					1758

<210> 3

<211> 919

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 3

Met	Glu	Val	Gln	Leu	Gly	Leu	Gly	Arg	Val	Tyr	Pro	Arg	Pro	Pro	Ser
1				5					10					15	
Lys	Thr	Tyr	Arg	Gly	Ala	Phe	Gln	Asn	Leu	Phe	Gln	Ser	Val	Arg	Glu
			20					25					30		
Val	Ile	Gln	Asn	Pro	Gly	Pro	Arg	His	Pro	Glu	Ala	Ala	Ser	Ala	Ala
			35					40					45		
Pro	Pro	Gly	Ala	Ser	Leu	Leu	Leu	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln
			50					55					60		
Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Glu	Thr
65					70					75					80
Ser	Pro	Arg	Gln	Gln	Gln	Gln	Gln	Gln	Gly	Glu	Asp	Gly	Ser	Pro	Gln
					85					90				95	
Ala	His	Arg	Arg	Gly	Pro	Thr	Gly	Tyr	Leu	Val	Leu	Asp	Glu	Glu	Gln
					100					105				110	
Gln	Pro	Ser	Gln	Pro	Gln	Ser	Ala	Leu	Glu	Cys	His	Pro	Glu	Arg	Gly
					115					120				125	
Cys	Val	Pro	Glu	Pro	Gly	Ala	Ala	Val	Ala	Ala	Ser	Lys	Gly	Leu	Pro
					130					135				140	
Gln	Gln	Leu	Pro	Ala	Pro	Pro	Asp	Glu	Asp	Asp	Ser	Ala	Ala	Pro	Ser
145						150				155					160
Thr	Leu	Ser	Leu	Leu	Gly	Pro	Thr	Phe	Pro	Gly	Leu	Ser	Ser	Cys	Ser
					165					170				175	
Ala	Asp	Leu	Lys	Asp	Ile	Leu	Ser	Glu	Ala	Ser	Thr	Met	Gln	Leu	Leu
					180					185				190	

Gln Gln Gln Gln Gln Glu Ala Val Ser Glu Gly Ser Ser Ser Gly Arg
 195 200 205
 Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser Lys Asp Asn Tyr Leu
 210 215 220
 Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys Glu Leu Cys Lys Ala
 225 230 235 240
 Val Ser Val Ser Met Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser
 245 250 255
 Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala Pro Leu Leu Gly
 260 265 270
 Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala Pro Leu Ala Glu Cys
 275 280 285
 Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys Ser Thr Glu Asp Thr
 290 295 300
 Ala Glu Tyr Ser Pro Phe Lys Gly Gly Tyr Thr Lys Gly Leu Glu Gly
 305 310 315 320
 Glu Ser Leu Gly Cys Ser Gly Ser Ala Ala Ala Gly Ser Ser Gly Thr
 325 330 335
 Leu Glu Leu Pro Ser Thr Leu Ser Leu Tyr Lys Ser Gly Ala Leu Asp
 340 345 350
 Glu Ala Ala Ala Tyr Gln Ser Arg Asp Tyr Tyr Asn Phe Pro Leu Ala
 355 360 365
 Leu Ala Gly Pro Pro Pro Pro Pro Pro Pro Pro His Pro His Ala Arg
 370 375 380
 Ile Lys Leu Glu Asn Pro Leu Asp Tyr Gly Ser Ala Trp Ala Ala Ala
 385 390 395 400
 Ala Ala Gln Cys Arg Tyr Gly Asp Leu Ala Ser Leu His Gly Ala Gly
 405 410 415
 Ala Ala Gly Pro Gly Ser Gly Ser Pro Ser Ala Ala Ala Ser Ser Ser
 420 425 430
 Trp His Thr Leu Phe Thr Ala Glu Glu Gly Gln Leu Tyr Gly Pro Cys
 435 440 445
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 450 455 460
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Glu Ala Gly Ala Val Ala Pro Tyr
 465 470 475 480
 Gly Tyr Thr Arg Pro Gln Gly Leu Ala Gly Gln Glu Ser Asp Phe
 485 490 495
 Thr Ala Pro Asp Val Trp Tyr Pro Gly Gly Met Val Ser Arg Val Pro
 500 505 510
 Tyr Pro Ser Pro Thr Cys Val Lys Ser Glu Met Gly Pro Trp Met Asp
 515 520 525
 Ser Tyr Ser Gly Pro Tyr Gly Asp Met Arg Leu Glu Thr Ala Arg Asp
 530 535 540
 His Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu
 545 550 555 560
 Ile Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys
 565 570 575
 Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys
 580 585 590
 Tyr Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg
 595 600 605
 Lys Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met
 610 615 620
 Thr Leu Gly Ala Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln
 625 630 635 640
 Glu Glu Gly Glu Ala Ser Ser Thr Thr Ser Pro Thr Glu Glu Thr Thr
 645 650 655
 Gln Lys Leu Thr Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile
 660 665 670

Phe Leu Asn Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly
 675 680 685
 His Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu
 690 695 700
 Asn Glu Leu Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys
 705 710 715 720
 Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val
 725 730 735
 Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg
 740 745 750
 Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu
 755 760 765
 Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys
 770 775 780
 Val Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr
 785 790 795 800
 Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile
 805 810 815
 Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met
 820 825 830
 Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn
 835 840 845
 Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp
 850 855 860
 Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu
 865 870 875 880
 Leu Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met Ala
 885 890 895
 Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys
 900 905 910
 Pro Ile Tyr Phe His Thr Gln
 915

<210> 4

<211> 4321

<212> DNA

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 4

cgagatcccg	gggagccagc	ttgctgggag	agcgggacgg	tccggagcaa	gcccacaggc	60
agaggaggcg	acagagggaa	aaagggccga	gctagccgct	ccagtgtgt	acaggagccg	120
aaggagcgca	ccacgccagc	cccagcccgg	ctccagcgac	agccaacgcc	tcttgacgag	180
cggcggcttc	gaagccgccc	cccggagctg	ccctttcctc	ttcgggtgaag	tttttaaaag	240
ctgctaaaga	ctcggaggaa	gcaaggaaaag	tgcttggtag	gactgacggc	tgccctttgtc	300
ctcctcctct	ccaccccggc	ttccccccacc	ctgccttccc	cccctccccc	gtctttctctc	360
ccgcagctgc	ctcagtcggc	tactctcagc	caacccccct	caccaccctt	ctccccaccc	420
gcccccccg	ccccgtcggc	ccagcgctgc	cagcccaggt	ttgcagagag	gtaactccct	480
ttggctgcga	gcgggcgagc	tagctgcaca	ttgcaaagaa	ggctcttagg	agccaggcga	540
ctggggagcg	gcttcagcac	tgacagccag	acccgcctgg	ttagaattcc	ggcggagaga	600
accctctgtt	ttcccccaat	ctctctccac	ctcctcctgc	cttccccacc	ccgagtgcgg	660
agcagagatc	aaaagatgaa	aaggcagtc	ggtcttcagt	agccaaaaaa	caaaacaaac	720
aaaaacaaaa	aagccgaaat	aaaagaaaaa	gataataact	cagttcttat	ttgcacctac	780
ttcagtgagc	actgaatttg	gaagggtggag	gattttgttt	ttttctttta	agatctgggc	840
atctttttgaa	tctacccttc	aagtattaa	agacagactg	tgagcctagc	agggcagatc	900
ttgtccaccg	tgtgtcttct	tctgcacgag	actttgaggc	tgctcagagc	ctttttgcgt	960
ggttgtctcc	gcaagtttcc	ttctctggag	cttcccgcag	gtgggcagct	agctgcagcg	1020
actaccgcat	catcacagcc	tggtgaactc	ttctgagcaa	gagaagggga	ggcggggtaa	1080

gggaagtagg	tggaagattc	agccaagctc	aaggatggaa	gtgcagttag	ggctgggaag	1140
ggtctaccct	cggccgccgt	ccaagaccta	cggaggagct	ttccagaatc	tggtccagag	1200
cgtgcgcgaa	gtgatccaga	acccgggccc	caggcaccca	gaggccgcga	gcgcagcacc	1260
tcccggcgcc	agtttgctgc	tgctgcagca	gcagcagcag	cagcagcagc	agcagcagca	1320
gcagcagcag	cagcagcagc	agcagcaaga	gactagcccc	aggcagcagc	agcagcagca	1380
gggtgaggat	ggttctcccc	aagcccatcg	tagaggcccc	acaggctacc	tggtcctgga	1440
tgaggaacag	caaccttcac	agccgcagtc	ggccctggag	tgccaccccg	agagagggtg	1500
cgtcccagag	cctggagccg	ccgtggccgc	cagcaagggg	ctgccgcagc	agctgccagc	1560
acctccggac	gaggatgact	cagctgcccc	atccacgttg	tccctgctgg	gccccacttt	1620
ccccggctta	agcagctgct	ccgtgacct	taaagacatc	ctgagcgagg	ccagcaccat	1680
gcaactcctt	cagcaacagc	agcaggaagc	agtatccgaa	ggcagcagca	gcgggagagc	1740
gagggaggcc	tcgggggctc	ccacttcctc	caaggacaat	tacttagggg	gcacttcgac	1800
catttctgac	aacgccaaag	agttgtgtaa	ggcagtgctc	gtgtccatgg	gcctgggtgt	1860
ggaggcggtt	gagcatctga	gtccaggggg	acagcttcgg	ggggattgca	tgtacgcccc	1920
acttttgga	gttccacccg	ctgtgcgtcc	cactccttgt	gccccattgg	ccgaatgcaa	1980
aggttctctg	ctagacgaca	gcgcaggcaa	gagcactgaa	gatactgctg	agtattcccc	2040
tttcaagggg	ggttacacca	aagggctaga	aggcgagagc	ctaggctgct	ctggcagcgc	2100
tgcagcaggg	agctccggga	cacttgaact	gccgtctacc	ctgtctctct	acaagtccgg	2160
agcactggac	gaggcagctg	cgtaccagag	tcgcgactac	tacaactttc	cactggctct	2220
ggccggaccg	cgcgccccct	cgccgcctcc	ccatccccac	gctcgcatac	agctggagaa	2280
cccgcctggc	tacggcagcg	cctgggcggc	tgccgcggcg	cagtgcgcgt	atggggacct	2340
ggcgagcctg	catggcgcg	gtgcagcggg	accgggttct	gggtcacctc	cagccgcgcg	2400
ttcctcatcc	tggcacactc	tcttcacagc	cgaagaaggc	cagttgtatg	gaccgtgtgg	2460
tggtggtggg	ggtggtggcg	gcggcgcgcg	cggcgcgcg	ggcgcgcgcg	gcggcgcgcg	2520
cggcgcgcg	gaggcgggag	ctgtagcccc	ctacggctac	actcggcccc	ctcaggggct	2580
ggcgggcccag	gaaagcgact	tcaccgcacc	tgatgtgtgg	taccctggcg	gcatgggtgag	2640
cagagtgcct	tatcccagtc	ccacttgtgt	caaaagcgaa	atgggccccct	ggatggatag	2700
ctactccgga	ccttacgggg	acatgcgttt	ggagactgcc	agggaccatg	ttttgccccat	2760
tgactattac	tttccacccc	agaagacctg	cctgatctgt	ggagatgaag	cttctgggtg	2820
tcactatgga	gctctcacat	gtggaagctg	caaggtcttc	ttcaaaagag	ccgctgaagg	2880
gaaacagaag	tacctgtgcg	ccagcagaaa	tgattgcact	attgataaat	tccgaaggaa	2940
aaattgtcca	tcttgtcgtc	ttcggaaatg	ttatgaagca	gggatgactc	tgggagcccc	3000
gaagctgaag	aaacttggtg	atctgaaact	acaggaggaa	ggagaggctt	ccagcaccac	3060
cagccccact	gaggagacaa	cccagaagct	gacagtgtca	cacattgaag	gctatgaatg	3120
tcagcccato	tttctgaatg	tcctggaagc	cattgagcca	ggtgtagtgt	gtgctggaca	3180
cgacaacaac	cagcccgaact	cctttgcagc	cctgtctctc	agcctcaatg	aactgggaga	3240
gagacagctt	gtacacgtgg	tcaagtgggc	caaggccttg	cctggcttcc	gcaacttaca	3300
cgtggacgac	cagatggctg	tcattcagta	ctcctggatg	gggctcatgg	tgtttgccat	3360
gggctggcga	tccttcacca	atgtcaactc	caggatgctc	tacttcgccc	ctgatctggt	3420
tttcaatgag	taccgcatgc	acaagtcccc	gatgtacagc	cagtgtgtcc	gaatgaggca	3480
cctctctcaa	gagtttggtg	ggctccaaat	cacccccag	gaattcctgt	gcatgaaagc	3540
actgctactc	ttcagcatta	ttccagtggg	tgggctgaaa	aatcaaaaat	tctttgatga	3600
acttcgaatg	aactacatca	aggaactcga	tcgtatcatt	gcatgcaaaa	gaaaaaatcc	3660
cacatcctgc	tcaagacgct	tctaccagct	caccaagctc	ctggactccg	tgcagcctat	3720
tgcgagagag	ctgcatcagt	tcacttttga	cctgctaate	aagtcacaca	tggtgagcgt	3780
ggactttccg	gaaatgatgg	cagagatcat	ctctgtgcaa	gtgccaaga	tcccttctgg	3840
gaaagtcaag	cccatctatt	tccacaccca	gtgaagcatt	ggaaacccta	tttccccacc	3900
ccagctcatg	ccccctttca	gatgtcttct	gcctgttata	actctgcact	actcctctgc	3960
agtgccttgg	ggaatttcc	ctattgatgt	acagtctgtc	atgaacatgt	tccatgaattc	4020
tatttgctgg	gctttttttt	tctctttctc	tcctttcttt	ttcttcttcc	ctccctatct	4080
aacctccca	tggcaccttc	agactttgct	tcccatgtgt	gctcctatct	gtgttttgaa	4140
tggtgttgta	tgcctttaaa	tctgtgatga	tcctcatatg	gcccagtgct	aagttgtgct	4200
tgtttacagc	actactctgt	gccagccaca	caaacgttta	cttatcttat	gccacgggaa	4260
gtttagagag	ctaagattat	ctggggaaat	caaaacaaaa	aacaagcaaa	caaaaaaaaa	4320
a						4321

<210> 5

<211> 433

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 5

```

Met Ser Gly Arg Pro Arg Thr Thr Ser Phe Ala Glu Ser Cys Lys Pro
 1          5          10          15
Val Gln Gln Pro Ser Ala Phe Gly Ser Met Lys Val Ser Arg Asp Lys
 20          25          30
Asp Gly Ser Lys Val Thr Thr Val Val Ala Thr Pro Gly Gln Gly Pro
 35          40          45
Asp Arg Pro Gln Glu Val Ser Tyr Thr Asp Thr Lys Val Ile Gly Asn
 50          55          60
Gly Ser Phe Gly Val Val Tyr Gln Ala Lys Leu Cys Asp Ser Gly Glu
 65          70          75          80
Leu Val Ala Ile Lys Lys Val Leu Gln Asp Lys Arg Phe Lys Asn Arg
 85          90          95
Glu Leu Gln Ile Met Arg Lys Leu Asp His Cys Asn Ile Val Arg Leu
100          105          110
Arg Tyr Phe Phe Tyr Ser Ser Gly Glu Lys Lys Asp Glu Val Tyr Leu
115          120          125
Asn Leu Val Leu Asp Tyr Val Pro Glu Thr Val Tyr Arg Val Ala Arg
130          135          140
His Tyr Ser Arg Ala Lys Gln Thr Leu Pro Val Ile Tyr Val Lys Leu
145          150          155          160
Tyr Met Tyr Gln Leu Phe Arg Ser Leu Ala Tyr Ile His Ser Phe Gly
165          170          175
Ile Cys His Arg Asp Ile Lys Pro Gln Asn Leu Leu Leu Asp Pro Asp
180          185          190
Thr Ala Val Leu Lys Leu Cys Asp Phe Gly Ser Ala Lys Gln Leu Val
195          200          205
Arg Gly Glu Pro Asn Val Ser Tyr Ile Cys Ser Arg Tyr Tyr Arg Ala
210          215          220
Pro Glu Leu Ile Phe Gly Ala Thr Asp Tyr Thr Ser Ser Ile Asp Val
225          230          235          240
Trp Ser Ala Gly Cys Val Leu Ala Glu Leu Leu Leu Gly Gln Pro Ile
245          250          255
Phe Pro Gly Asp Ser Gly Val Asp Gln Leu Val Glu Ile Ile Lys Val
260          265          270
Leu Gly Thr Pro Thr Arg Glu Gln Ile Arg Glu Met Asn Pro Asn Tyr
275          280          285
Thr Glu Phe Lys Phe Pro Gln Ile Lys Ala His Pro Trp Thr Lys Asp
290          295          300
Ser Ser Gly Thr Gly His Phe Thr Ser Gly Val Arg Val Phe Arg Pro
305          310          315          320
Arg Thr Pro Pro Glu Ala Ile Ala Leu Cys Ser Arg Leu Leu Glu Tyr
325          330          335
Thr Pro Thr Ala Arg Leu Thr Pro Leu Glu Ala Cys Ala His Ser Phe
340          345          350
Phe Asp Glu Leu Arg Asp Pro Asn Val Lys Leu Pro Asn Gly Arg Asp
355          360          365
Thr Pro Ala Leu Phe Asn Phe Thr Thr Gln Glu Leu Ser Ser Asn Pro
370          375          380
Pro Leu Ala Thr Ile Leu Ile Pro Pro His Ala Arg Ile Gln Ala Ala
385          390          395          400
Ala Ser Thr Pro Thr Asn Ala Thr Ala Ala Ser Asp Ala Asn Thr Gly
405          410          415
Asp Arg Gly Gln Thr Asn Asn Ala Ala Ser Ala Ser Ala Ser Asn Ser
420          425          430
Thr

```

<210> 6

<211> 1639

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 6

atcatctata	tggttaatat	ccgtgccgat	ctgtcttgaa	ggagaaatat	atcgcttggt	60
ttgtttttta	tagtatataa	aaggagtga	aagccaagag	gacgaagtct	ttttcttttt	120
cttctgtggg	agaacttaat	gctgcattta	tcgttaacct	aacaccccaa	cataaagaca	180
aaaggaagaa	aaggaggaag	gaaggaaaag	gtgattcgcg	aagagagtga	tcattgtcagg	240
gcggtccaga	accacctcct	ttgcggagag	ctgcaagccg	gtgcagcagc	cttcagcttt	300
tggcagcatg	aaagttagca	gagacaagga	cggcagcaag	gtgacaacag	tgggtggcaac	360
tcctgggcag	ggtccagaca	ggccacaaga	agtcagctat	acagacacta	aagtgtattgg	420
aatggatca	tttgggtgtg	tatatcaagc	caaactttgt	gattcaggag	aactgggtcgc	480
catcaagaaa	gtattgcagg	acaagagatt	taagaatcga	gagctccaga	tcattgagaaa	540
gctagatcac	tgtaacatag	tccgattgcg	ttatttcttc	tactccagtg	gtgagaagaa	600
agatgaggtc	tattcttaatc	tgggtgctgga	ctatgttccg	gaaacagtat	acagagttgc	660
cagacactat	agtcgagcca	aacagacgct	ccctgtgatt	tatgtcaagt	tgtatatgta	720
tcagctgttc	cgaagtttag	cctatatcca	ttcctttgga	atctgccatc	gggatattaa	780
accgcagaac	ctctgtgttg	atcctgatac	tgtctgatta	aaactctgtg	actttggaag	840
tgcaaagcag	ctgggtccgag	gagaacccaa	tgtttcgtat	atctgttctc	ggtactatag	900
ggcaccagag	ttgatctttg	gagccactga	ttatacctct	agtatagatg	tatgggtctgc	960
tggctgtgtg	ttggctgagc	tggtactagg	acaaccaata	tttccagggg	atagtgggtgt	1020
ggatcagttg	gtagaaataa	tcaaggctct	gggaactcca	acaagggagc	aaatcagaga	1080
aatgaaccga	aactacacag	aattttaaatt	ccctcaaatt	aaggcacatc	cttggaactaa	1140
ggattcgtca	ggaacaggac	atttcacctc	aggagtgcgg	gtcttccgac	cccgaactcc	1200
accggaggca	attgcactgt	gtagccgtct	gctggagtat	acaccaactg	cccgaactaac	1260
accactggaa	gcttgtgcac	attcattttt	tgatgaatta	cgggacccaa	atgtcaaact	1320
accaaattgg	cgagacacac	ctgcactctt	caacttcacc	actcaagaac	tgtcaagtaa	1380
tccacctctg	gctaccatcc	ttattcctcc	tcattgtcgg	attcaagcag	ctgcttcaac	1440
ccccacaaat	gccacagcag	cgtcagatgc	taatactgga	gaccgtggac	agaccaataa	1500
tgctgcttct	gcattcagct	ccaactccac	ctgaacagtc	ccgagcagcc	agctgcacag	1560
gaaaaaccac	cagttacttg	agtgtcactc	agcaacactg	gtcacgtttg	gaaagaatat	1620
taaaaaaaaa	aaaaaaaaa					1639

<210> 7

<211> 391

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 7

Met	Lys	Cys	Leu	Val	Thr	Gly	Gly	Asn	Val	Lys	Val	Leu	Gly	Lys	Ala
1				5				10						15	
Val	His	Ser	Leu	Ser	Arg	Ile	Gly	Asp	Glu	Leu	Tyr	Leu	Glu	Pro	Leu
		20						25					30		
Glu	Asp	Gly	Leu	Ser	Leu	Arg	Thr	Val	Asn	Ser	Ser	Arg	Ser	Ala	Tyr
		35					40					45			
Ala	Cys	Phe	Leu	Phe	Ala	Pro	Leu	Phe	Phe	Gln	Gln	Tyr	Gln	Ala	Ala
	50					55				60					
Thr	Pro	Gly	Gln	Asp	Leu	Leu	Arg	Cys	Lys	Ile	Leu	Met	Lys	Ser	Phe
65					70					75					80

Leu Ser Val Phe Arg Ser Leu Ala Met Leu Glu Lys Thr Val Glu Lys
 85 90 95
 Cys Cys Ile Ser Leu Asn Gly Arg Ser Ser Arg Leu Val Val Gln Leu
 100 105 110
 His Cys Lys Phe Gly Val Arg Lys Thr His Asn Leu Ser Phe Gln Asp
 115 120 125
 Cys Glu Ser Leu Gln Ala Val Phe Asp Pro Ala Ser Cys Pro His Met
 130 135 140
 Leu Arg Ala Pro Ala Arg Val Leu Gly Glu Ala Val Leu Pro Phe Ser
 145 150 155 160
 Pro Ala Leu Ala Glu Val Thr Leu Gly Ile Gly Arg Gly Arg Val
 165 170 175
 Ile Leu Arg Ser Tyr His Glu Glu Glu Ala Asp Ser Thr Ala Lys Ala
 180 185 190
 Met Val Thr Glu Met Cys Leu Gly Glu Glu Asp Phe Gln Gln Leu Gln
 195 200 205
 Ala Gln Glu Gly Val Ala Ile Thr Phe Cys Leu Lys Glu Phe Arg Gly
 210 215 220
 Leu Leu Ser Phe Ala Glu Ser Ala Asn Leu Asn Leu Ser Ile His Phe
 225 230 235 240
 Asp Ala Pro Gly Arg Pro Ala Ile Phe Thr Ile Lys Asp Ser Leu Leu
 245 250 255
 Asp Gly His Phe Val Leu Ala Thr Leu Ser Asp Thr Asp Ser His Ser
 260 265 270
 Gln Asp Leu Gly Ser Pro Glu Arg His Gln Pro Val Pro Gln Leu Gln
 275 280 285
 Ala His Ser Thr Pro His Pro Asp Asp Phe Ala Asn Asp Asp Ile Asp
 290 295 300
 Ser Tyr Met Ile Ala Met Glu Thr Thr Ile Gly Asn Glu Gly Ser Arg
 305 310 315 320
 Val Leu Pro Ser Ile Ser Leu Ser Pro Gly Pro Gln Pro Pro Lys Ser
 325 330 335
 Pro Gly Pro His Ser Glu Glu Glu Asp Glu Ala Glu Pro Ser Thr Val
 340 345 350
 Pro Gly Thr Pro Pro Pro Lys Lys Phe Arg Ser Leu Phe Phe Gly Ser
 355 360 365
 Ile Leu Ala Pro Val Arg Ser Pro Gln Gly Pro Ser Pro Val Leu Ala
 370 375 380
 Glu Asp Ser Glu Gly Glu Gly
 385 390

<210> 8

<211> 2102

<212> DNA

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 8

gcgcgggaag	ggaccccgga	cccggaggtc	gcggagagct	gggcagtgtt	ggccgctggc	60
ggagcgctgg	ggcagcatga	agtgcctggt	cacgggcggc	aacgtgaagg	tgctcggcaa	120
ggccgtccac	tccctgtccc	gcacgcggga	cgagctctac	ctggaaccct	tgaggacgg	180
gctctccctc	cggacggtga	actcctcccg	ctctgcctat	gcctgctttc	tctttgcccc	240
gctcttcttc	cagcaatacc	aggcagccac	ccctggtcag	gacctgctgc	gctgtaagat	300
cctgatgaag	tctttcctgt	ctgtcttccg	ctcactggcg	atgctggaga	agacgggtgga	360
aaaatgctgc	atctccctga	atggccggag	cagccgcctg	gtgggtccagc	tgcattgcaa	420
gttcgggggtg	cgggaagactc	acaacctgtc	cttccaggac	tgtgagtccc	tgcaggccgt	480
cttcgaccca	gcctcgtgcc	cccacatgct	ccgcgcccca	gcacgggttc	tgggggaggc	540
tggtctgccc	ttctctcctg	cactggctga	agtgacgctg	ggcattggcc	gtggccgcag	600

```

ggatcatcctg cgcagctacc acgaggagga ggcagacagc actgccaaag ccatgggtgac 660
tgagatgtgc cttgggagagg aggattttcca gcagctgcag gccaggaag ggggtggccat 720
cacttttctgc ctcaaggaat tccggggggt cctgagcttt gcagagtcag caaacttgaa 780
tcttagcatt cattttgatg ctccaggcag gcccgccatc ttcacatca aggactcttt 840
gctggacggc cactttgtct tggccacact ctcagacacc gactcgcaact cccaggacct 900
gggctcccca gagcgtcacc agccagtgc ttagctccag gctcacagca caccacaccc 960
ggacgacttt gccaatgacg acattgactc ttacatgac gccatggaaa cactatagg 1020
caatgagggc tcgcggtgct tgccctccat ttccctttca cctggccccc agcccccaa 1080
gagccccgt cccactccg aggaggaaga tgaggctgag cccagtacag tgcctgggac 1140
tccccaccc aagaagttcc gctcactgtt cttcggtcc atcctggccc ctgtacgctc 1200
ccccagggc cccagccctg tgctggcgga agacagtgc ggtgaaggct gaaccaagaa 1260
cctgaagcct gtacccagag gccttggaact agacgaagcc ccagccagtgc gcagaactgg 1320
gtctctcagc cctggggatc agaaagggtg gcttgctgga gctgagctgt ttcactgctt 1380
ctcgacggc ccagctggct gtcactgtaa agctgtccca cagcggtcgg gcctggggcg 1440
ttatctcccc acaaccccca gccaatcagg actttccaga cttggccctg aactactgac 1500
gttcctacct cttattttctc attgagcctc aggtatact ccagctggcc aaggctggaa 1560
acctgtctcc ctcaggctca ccttcctaag gaaaatgtca tagtaggtgc tgctggcccc 1620
tggtgatcca gcttctctgc caatcatgac ctgttccttc ctgaagtcct gggcatgcat 1680
ctgggacccc cgtggagctg acaagttttc cttgctttcc tgatactctt tggcgctgac 1740
ttggaattct aagagccttg gacccgagtg tgtggctagg gttgccctgg ctggggcccc 1800
gtgccgagac tcccaagcgg ctctgtgcag aagagctgcc aggcagtgtc ttagatgtga 1860
gacggaggcc atggcgagaa tccagctttg acctttattc aagagaccag atgggttgcc 1920
ccaggatccg gctgccagcc ctgaggccaa gcacggctgg agaccacga cctggcctgc 1980
cgttgccctg agctgcagcc tcggccccag gatcctgctc acagtcaccg cagggtgcagg 2040
caggaagcag ccctggggga ctggacgctg ctattgattc attaaaaaa gaaaagaaaa 2100
at 2102

```

<210> 9

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 9

gggcccctgg atggatagct ac

22

<210> 10

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 10

gtagctatcc atccaggggc c

21

<210> 11

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 11

gggccccctgg atggatagct acctcgaggt agctatccat ccaggggcc

49

<210> 12

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 12

tttttgggcc cctggatgga tagctacctc gaggtagcta tccatccagg ggcc

54

<210> 13

<211> 483

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 13

Met	Ala	Thr	Ile	Glu	Glu	Ile	Ala	His	Gln	Ile	Ile	Glu	Gln	Gln	Met
1				5					10					15	
Gly	Glu	Ile	Val	Thr	Glu	Gln	Gln	Thr	Gly	Gln	Lys	Ile	Gln	Ile	Val
			20					25					30		
Thr	Ala	Leu	Asp	His	Asn	Thr	Gln	Gly	Lys	Gln	Phe	Ile	Leu	Thr	Asn
		35					40				45				
His	Asp	Gly	Ser	Thr	Pro	Ser	Lys	Val	Ile	Leu	Ala	Arg	Gln	Asp	Ser
	50					55					60				
Thr	Pro	Gly	Lys	Val	Phe	Leu	Thr	Thr	Pro	Asp	Ala	Ala	Gly	Val	Asn
65					70					75				80	
Gln	Leu	Phe	Phe	Thr	Thr	Pro	Asp	Leu	Ser	Ala	Gln	His	Leu	Gln	Leu
				85					90					95	
Leu	Thr	Asp	Asn	Ser	Pro	Asp	Gln	Gly	Pro	Asn	Lys	Val	Phe	Asp	Leu
			100					105					110		
Cys	Val	Val	Cys	Gly	Asp	Lys	Ala	Ser	Gly	Arg	His	Tyr	Gly	Ala	Val
		115					120					125			
Thr	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Lys	Arg	Ser	Ile	Arg	Lys	Asn
	130					135					140				
Leu	Val	Tyr	Ser	Cys	Arg	Gly	Ser	Lys	Asp	Cys	Ile	Ile	Asn	Lys	His
145					150					155					160
His	Arg	Asn	Arg	Cys	Gln	Tyr	Cys	Arg	Leu	Gln	Arg	Cys	Ile	Ala	Phe
				165					170						175
Gly	Met	Lys	Gln	Asp	Ser	Val	Gln	Cys	Glu	Arg	Lys	Pro	Ile	Glu	Val
			180					185					190		
Ser	Arg	Glu	Lys	Ser	Ser	Asn	Cys	Ala	Ala	Ser	Thr	Glu	Lys	Ile	Tyr
		195					200					205			
Ile	Arg	Lys	Asp	Leu	Arg	Ser	Pro	Leu	Thr	Ala	Thr	Pro	Thr	Phe	Val
	210					215					220				
Thr	Asp	Ser	Glu	Ser	Thr	Arg	Ser	Thr	Gly	Leu	Leu	Asp	Ser	Gly	Met
225					230					235					240
Phe	Met	Asn	Ile	His	Pro	Ser	Gly	Val	Lys	Thr	Glu	Ser	Ala	Val	Leu
				245					250					255	
Met	Thr	Ser	Asp	Lys	Ala	Glu	Ser	Cys	Gln	Gly	Asp	Leu	Ser	Thr	Leu
			260					265					270		
Ala	Asn	Val	Val	Thr	Ser	Leu	Ala	Asn	Leu	Gly	Lys	Thr	Lys	Asp	Leu
			275				280						285		

```

Ser Gln Asn Ser Asn Glu Met Ser Met Ile Glu Ser Leu Ser Asn Asp
290                295                300
Asp Thr Ser Leu Cys Glu Phe Gln Glu Met Gln Thr Asn Gly Asp Val
305                310                315                320
Ser Arg Ala Phe Asp Thr Leu Ala Lys Ala Leu Asn Pro Gly Glu Ser
                325                330                335
Thr Ala Cys Gln Ser Ser Val Ala Gly Met Glu Gly Ser Val His Leu
                340                345                350
Ile Thr Gly Asp Ser Ser Ile Asn Tyr Thr Glu Lys Glu Gly Pro Leu
                355                360                365
Leu Ser Asp Ser His Val Ala Phe Arg Leu Thr Met Pro Ser Pro Met
                370                375                380
Pro Glu Tyr Leu Asn Val His Tyr Ile Gly Glu Ser Ala Ser Arg Leu
385                390                395                400
Leu Phe Leu Ser Met His Trp Ala Leu Ser Ile Pro Ser Phe Gln Ala
                405                410                415
Leu Gly Gln Glu Asn Ser Ile Ser Leu Val Lys Ala Tyr Trp Asn Glu
                420                425                430
Leu Phe Thr Leu Gly Leu Ala Gln Cys Trp Gln Val Met Asn Val Ala
                435                440                445
Thr Ile Leu Ala Thr Phe Val Asn Cys Leu His Asn Ser Leu Gln Gln
                450                455                460
Asp Ala Lys Val Ile Ala Ala Leu Ile His Phe Thr Arg Arg Ala Ile
465                470                475                480
Thr Asp Leu

```

<210> 14

<211> 596

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 14

```

Met Thr Ser Pro Ser Pro Arg Ile Gln Ile Ile Ser Thr Asp Ser Ala
1                5                10                15
Val Ala Ser Pro Gln Arg Ile Gln Ile Val Thr Asp Gln Gln Thr Gly
                20                25                30
Gln Lys Ile Gln Ile Val Thr Ala Val Asp Ala Ser Gly Ser Pro Lys
                35                40                45
Gln Gln Phe Ile Leu Thr Ser Pro Asp Gly Ala Gly Thr Gly Lys Val
50                55                60
Ile Leu Ala Ser Pro Glu Thr Ser Ser Ala Lys Gln Leu Ile Phe Thr
65                70                75                80
Thr Ser Asp Asn Leu Val Pro Gly Arg Ile Gln Ile Val Thr Asp Ser
                85                90                95
Ala Ser Val Glu Arg Leu Leu Gly Lys Thr Asp Val Gln Arg Pro Gln
                100                105                110
Val Val Glu Tyr Cys Val Val Cys Gly Asp Lys Ala Ser Gly Arg His
                115                120                125
Tyr Gly Ala Val Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Ser
130                135                140
Val Arg Lys Asn Leu Thr Tyr Ser Cys Arg Ser Asn Gln Asp Cys Ile
145                150                155                160
Ile Asn Lys His His Arg Asn Arg Cys Gln Phe Cys Arg Leu Lys Lys
                165                170                175
Cys Leu Glu Met Gly Met Lys Met Glu Ser Val Gln Ser Glu Arg Lys
                180                185                190

```

```

Pro Phe Asp Val Gln Arg Glu Lys Pro Ser Asn Cys Ala Ala Ser Thr
    195                200                205
Glu Lys Ile Tyr Ile Arg Lys Asp Leu Arg Ser Pro Leu Ile Ala Thr
    210                215                220
Pro Thr Phe Val Ala Asp Lys Asp Gly Ala Arg Gln Thr Gly Leu Leu
    225                230                235                240
Asp Pro Gly Met Leu Val Asn Ile Gln Gln Pro Leu Ile Arg Glu Asp
    245                250                255
Gly Thr Val Leu Leu Ala Thr Asp Ser Lys Ala Glu Thr Ser Gln Gly
    260                265                270
Ala Leu Gly Thr Leu Ala Asn Val Val Thr Ser Leu Ala Asn Leu Ser
    275                280                285
Glu Ser Leu Asn Asn Gly Asp Thr Ser Glu Ile Gln Pro Glu Asp Gln
    290                295                300
Ser Ala Ser Glu Ile Thr Arg Ala Phe Asp Thr Leu Ala Lys Ala Leu
    305                310                315                320
Asn Thr Thr Asp Ser Ser Ser Ser Pro Ser Leu Ala Asp Gly Ile Asp
    325                330                335
Thr Ser Gly Gly Gly Ser Ile His Val Ile Ser Arg Asp Gln Ser Thr
    340                345                350
Pro Ile Ile Glu Val Glu Gly Pro Leu Leu Ser Asp Thr His Val Thr
    355                360                365
Phe Lys Leu Thr Met Pro Ser Pro Met Pro Glu Tyr Leu Asn Val His
    370                375                380
Tyr Ile Cys Glu Ser Ala Ser Arg Leu Leu Phe Leu Ser Met His Trp
    385                390                395                400
Ala Arg Ser Ile Pro Ala Phe Gln Ala Leu Gly Gln Asp Cys Asn Thr
    405                410                415
Ser Leu Val Arg Ala Cys Trp Asn Glu Leu Phe Thr Leu Gly Leu Ala
    420                425                430
Gln Cys Ala Gln Val Met Ser Leu Ser Thr Ile Leu Ala Ala Ile Val
    435                440                445
Asn His Leu Gln Asn Ser Ile Gln Glu Asp Lys Leu Ser Gly Asp Arg
    450                455                460
Ile Lys Gln Val Met Glu His Ile Trp Lys Leu Gln Glu Phe Cys Asn
    465                470                475                480
Ser Met Ala Lys Leu Asp Ile Asp Gly Tyr Glu Tyr Ala Tyr Leu Lys
    485                490                495
Ala Ile Val Leu Phe Ser Pro Asp His Pro Gly Leu Thr Ser Thr Ser
    500                505                510
Gln Ile Glu Lys Phe Gln Glu Lys Ala Gln Met Glu Leu Gln Asp Tyr
    515                520                525
Val Gln Lys Thr Tyr Ser Glu Asp Thr Tyr Arg Leu Ala Arg Ile Leu
    530                535                540
Val Arg Leu Pro Ala Leu Arg Leu Met Ser Ser Asn Ile Thr Glu Glu
    545                550                555                560
Leu Phe Phe Thr Gly Leu Ile Gly Asn Val Ser Ile Asp Ser Ile Ile
    565                570                575
Pro Tyr Ile Leu Lys Met Glu Thr Ala Glu Tyr Asn Gly Gln Ile Thr
    580                585                590
Gly Ala Ser Leu
    595

```

<210> 15

<211> 2029

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 15
gaattcgggc ccgtcggcctt tcttcaaccc tctcttcccg gagcgccccc aatccacgag 60
tggcagccgc gggactgtcg cgtcggcgcc cgacgcggag tcagcagggg cgaaaagcgg 120
tagatcatgg caacctatga agaaattgca catcaaatta ttgaacaaca gatgggagag 180
attgttacag agcagcaaac tgggcagaaa atccagattg tgacagcact tgatcataat 240
acccaaggca agcagttcat tctgacaaat cagcagcggt ctactccaag caaagtcatt 300
ctggccaggc aagattccac tccgggaaaa gttttcctta caactccaga tgcagcaggt 360
gtcaaccagt tatttttttac cactcctgat ctgtctgcac aacacctgca gctcctaaca 420
gataattctc cagaccaagg accaaataag gtttttgatc tttgcgtagt atgtggagac 480
aaagcatcag gacgtcatta tggagcagta acttgtgaag gctgcaaagg attttttaaa 540
agaagcatcc gaaaaaattt agtatattca tgtcgaggat caaaggattg tattattaat 600
aagcaccacc gaaaccgctg tcaatactgc aggttacaga gatgtattgc gtttggaaatg 660
aagcaagact ctgtccaatg tgaaagaaaa cccattgaag tatcacgaga aaaatcttcc 720
aactgtgccg cttcaacaga aaaaatctat atccgaaagg accttcgtag cccattaact 780
gcaactccaa cttttgtaac agatagtga agtacaagg caacaggact gttagattca 840
ggaatgttca tgaatatcca tccatctgga gtaaaaactg agtcagctgt gctgatgaca 900
tcagataagg ctgaatcatg tcagggagat ttaagtacat tggccaatgt gggttacatca 960
ttagcgaatc ttggaaaaac taaagatctt tctcaaaata gtaatgaaa gtctatgatt 1020
gaaagcttaa gcaatgatga tacctctttg tgtgaatttc aagaaatgca gaccaacggt 1080
gatgtttcaa gggcatttga cactcttgca aaagcattga atcctggaga gagcacagcc 1140
tgccagagct cagtagcggg catggaagga agtgtacacc taatcactgg agattcaagc 1200
ataaattaca ccgaaaaaga ggggccactt ctcagcgatt cacatgtagc tttcaggctc 1260
accatgcctt ctccatgcc tgagtacctg aatgtgcact acattgggga gtctgcctcc 1320
agactgtgt tcttatcaat gcaactggga ctttcgatcc cttctttcca ggctctaggg 1380
caagaaaaca gcatatcact ggtgaaagct tactggaatg aactttttac tcttggtctt 1440
gccagtgct ggcaagtgat gaatgtagca actatattag caacatttgt caattgtctt 1500
cacaatagtc ttcaacaaga tgccaaggta attgcagccc tcattcattt cacaagaaga 1560
gcaatcactg atttataaat gcttaactat agaattggct atgactaccc aaaacagtg 1620
cccatacaaa aatgggggaaa attgcctttt gagctcagga ataatttata aattggggac 1680
taccttttag ttcttttagc tattctatct cttattgttt tatataattt ttaaatcatt 1740
tgcttctctc ttatgtttta cagcagaggg gtaatcacct taaaatgtca tcaaaaatag 1800
atctactaga aggcagcatc acattcccat cttacttatg gactcctacc cctgggtcat 1860
gtcttatatg cctgtaatgg ttataaagcc taccttcagg aaagctatgg ttgactaatt 1920
actaatggat ggggttttaa catgtccctc tacaataaat taaaatcttt caatgtttga 1980
atataatgtg gaggtgttta cctgagggcc tctctatctc cccgaattc 2029

<210> 16

<211> 6450

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 16

gagttgtgcc tggagtgtatg ttttaagccaa tgtcagggca aggcaacagt ccctggccgt 60
cctccagcac ctttgtaatg catatgagct cgggagacca gtacttaaag ttggaggccc 120
gggagccag gagctggcgg agggcggtcg tccctgggagc tgcaattgct ccgtcgggtc 180
gccggcttca ccggaccgca ggctcccggg gcagggccgg ggccagagct cgcgtgtcgg 240
cgggacatgc gctgcgtgc ctctaaccctc gggctgtgct ctttttccag gtggcccgcc 300
ggtttctgag ccttctgccc tgcggggaca cggctcgcac cctgcccgcg gccacggacc 360
atgaccatga ccctccacac caaagcatct gggatggccc tactgcatca gatccaaggg 420
aacgagctgg agccctgaa ccgtccgag ctcaagatcc cctggagcg gccctgggc 480
gaggtgtacc tggacagcag caagcccgc gtgtacaact accccgagg cgccgcctac 540
gagttcaacg ccgcggccgc cgccaacgcg caggtctacg gtcagaccgg cctcccctac 600
ggccccgggt ctgaggtgc ggcgttcggc tccaacggcc tgggggggtt cccccactc 660
aacagcgtgt ctccgagccc gctgatgcta ctgcacccgc cgccgagct gtcgcctttc 720
ctgcagcccc acggccagca ggtgccctac tacctggaga acgagcccag cggctacag 780
gtgcgcgagg ccggcccgcc ggcattctac aggccaaatt cagataatcg acgccagggt 840

ggcagagaaa	gattggccag	taccaatgac	aaggggaagta	tggctatgga	atctgccaa	900
gagactcgct	actgtgcagt	gtgcaatgac	tatgcttcag	gctaccatta	tggagtctgg	960
tcctgtgagg	gctgcaaggc	cttcttcaag	agaagtattc	aaggacataa	cgactatatg	1020
tgcccagcca	ccaaccagtg	caccattgat	aaaaaacagg	ggaagagctg	ccaggcctgc	1080
cggtccgca	aatgctacga	agtgggaatg	atgaaagggtg	ggatacgaaa	agaccgaaga	1140
ggagggagaa	tgttgaaaca	caagcgccag	agagatgatg	gggagggcag	gggtgaagtg	1200
gggtctgctg	gagacatgag	agctgccaac	ctttggccaa	gcccgtctcat	gatcaaacgc	1260
tctaagaaga	acagcctggc	cttgtccctg	acggccgacc	agatgggtcag	tgccttggtg	1320
gatgctgagc	ccccatact	ctattccgag	tatgatccta	ccagaccctt	cagtgaagct	1380
tcgatgatgg	gcttactgac	caacctggca	gacagggagc	tggttcacat	gatcaactgg	1440
gcgaagaggg	tgccaggctt	tgtggatttg	accctccatg	atcagggtcca	ccttctagaa	1500
tgtgcctggc	tagagatcct	gatgattggg	ctcgtctggc	gctccatgga	gcaccagtg	1560
aagctactgt	ttgctcctaa	cttgctcttg	gacaggaacc	agggaaaatg	tgtagagggc	1620
atgggtggaga	tcttcgacat	gctgctggct	acatcatctc	ggttccgcat	gatgaatctg	1680
cagggagagg	agtttgtgtg	cctcaaactc	attattttgc	ttaattcttg	agtgtacaca	1740
tttctgtcca	gcaccctgaa	gtctctggaa	gagaaggacc	atatccaccg	agtcctggac	1800
aagatcacag	acactttgat	ccacctgatg	gccaaaggcag	gcctgaccct	gcagcagcag	1860
caccagcggc	tgccccagct	cctcctcatc	ctctcccaca	tcaggcacat	gagtaacaaa	1920
ggcatggagc	atctgtacag	catgaagtgc	aagaacgtgg	tgccccctcta	tgacctgctg	1980
ctggagatgc	tggaagccca	ccgcctacat	gcgcccacta	gccgtggagg	ggcatccgtg	2040
gaggagacgg	accaaaagcca	cttggccact	gcgggctcta	cttcacgca	ttccttgcaa	2100
aagtattaca	tcacggggga	ggcagagggt	ttccctgcca	cagtctgaga	gctccctggc	2160
tcccacacgg	ttcagataat	ccctgctgca	ttttaccctc	atcatgcacc	acttttagcca	2220
aattctgtct	cctgcataca	ctccggcatg	catccaacac	caatggcttt	ctagatgagt	2280
ggccattcat	ttgcttgctc	agttcttagt	ggcacatctt	ctgtcttctg	ttgggaacag	2340
ccaaagggat	tccaaggcta	aatctttgta	acagctctct	ttcccccttg	ctatgttact	2400
aagcgtgagg	attcccgtag	ctcttcacag	ctgaactcag	tctatgggtt	ggggctcaga	2460
taactctgtg	catttaagct	acttgtagag	accaggcct	ggagagtaga	cattttgcct	2520
ctgataagca	ctttttaaat	ggctctaaga	ataagccaca	gcaaagaatt	taaagtggct	2580
cccttaattg	gtgacttgga	gaaagctagg	tcaaggggtt	attatagcac	cctcttgat	2640
tcctatggca	atgcatcctt	ttatgaaagt	ggtacacctt	aaagctttta	tatgactgta	2700
gcagagtatc	tggtgattgt	caattcactt	ccccctatag	gaatacaagg	ggccacacag	2760
ggaaggcaga	tcccctagtt	ggccaagact	tatttttaact	tgatacactg	cagattcaga	2820
gtgtcctgaa	gctctgcctc	tggctttccg	gtcatgggtt	ccagttaatt	catgcctccc	2880
atggacctat	ggagagcaac	aagttgatct	tagttaagtc	tccctatatg	agggataagt	2940
tcctgatttt	tgtttttatt	tttgtgttac	aaaagaaagc	cctccctccc	tgaacttgca	3000
gtaaggctcag	cttcaggacc	tgttccagtg	ggcactgtac	ttggatcttc	ccggcgtgtg	3060
tgtgccttac	acaggggtga	actgttcact	gtgggtgatg	atgatgaggg	taaagtgtag	3120
ttgaaaggag	caggggccct	ggtgttgcat	ttagccctgg	ggcatggagc	tgaacagtac	3180
ttgtgcagga	ttgttggggc	tactagagaa	caagaggggaa	agtagggcag	aaactggata	3240
cagttctgag	cacagccaga	cttgctcagg	tggccctgca	caggctgcag	ctacctagga	3300
acattccttg	cagaccccg	attgcctttg	ggggtgccc	gggatccctg	gggtagtcca	3360
gctcttattc	atctccagc	gtggccctgg	ttggaagaag	cagctgtcaa	ggtgtagaca	3420
gctgtgttcc	tacaattggc	ccagcacctt	ggggcacggg	agaaggggtg	ggaccgttgc	3480
tgtcactact	caggctgact	ggggcctggg	cagattacgt	atgcccttgg	tggtttagag	3540
ataatccaaa	atcagggttt	ggtttgggga	agaaaaatct	cccccttccc	cccccgcccc	3600
gttccctacc	gcctccactc	ctgccagctc	atttccttca	atttcctttg	acctataggc	3660
taaaaaagaa	aggctcattc	cagccacagg	gcagccttcc	ctgggccttt	gcttctctag	3720
cacaattatg	ggttacttcc	tttttcttaa	caaaaaagaa	tgtttgattt	cctctgggtg	3780
accttattgt	ctgtaattga	aacctatttg	agaggtgatg	tctgtgttag	ccaatgacct	3840
aggtagctgc	tcgggcttct	cttggtatgt	cttggttgga	aaagtggatt	tcattcattt	3900
ctgattgtcc	agttaagtga	tcaccaaagg	actgagaatc	tgggagggca	aaaaaaaaaa	3960
aaaaagtttt	tatgtgcact	taaatttggg	gacaatttta	tgtatctgtg	ttaaggatat	4020
gcttaagaac	ataattcttt	tgttgctggt	tgtttaagaa	gcaccttagt	ttgtttaaga	4080
agcaccttat	atagtataat	atatattttt	ttgaaattac	attgcttgtt	tatcacagaa	4140
tgaaatgtag	taattctggt	ctggatttaa	tttgactggg	ttaacatgca	aaaaccaagg	4200
aaaaatattt	agtttttttt	tttttttttg	tatacttttc	aagctacctt	gtcatgtata	4260
cagtcattta	tgccataaag	ctgggtgatta	ttcattttaaa	tgaagatcac	atctcatatc	4320
aacttttcta	tccacagtag	acaaaatagc	actaatccag	atgcctattg	ttggatattg	4380
aatgacagac	aatcttatgt	agcaaagatt	atgcctgaaa	aggaaaatta	ttcagggcag	4440
ctaattttgc	ttttacaaaa	atatcagtag	taatatTTTT	ggacagtagc	taatgggtca	4500

gtgggttctt	tttaatgttt	atacttagat	tttcttttaa	aaaaattaaa	ataaaacaaa	4560
aaaaatctt	aggactagac	gatgtaatac	cagctaaagc	caaacaatta	tacagtggaa	4620
ggttttacat	tattcatcca	atgtgtttct	attcatgtta	agatactact	acatttgaag	4680
tgggcagaga	acatcagatg	attgaaatgt	tgcgccaggg	gtctccagca	actttggaaa	4740
tctctttgta	tttttacttg	aagtgccact	aatggacagc	agatattttc	tggctgatgt	4800
tgtatttggg	tgtaggaaca	tgatttaaaa	aaaaaactct	tgctctgct	ttccccact	4860
ctgaggcaag	ttaaaatgta	aaagatgtga	tttatctggg	gggctcaggt	atgggtggga	4920
agtggattca	ggaatctggg	gaatggcaaa	tatattaaga	agagtattga	aagtatttgg	4980
aggaaaatgg	ttaattctgg	gtgtgcacca	aggttcagta	gagtccactt	ctgccttgga	5040
gaccacaaat	caactagctc	cattttacagc	cattttctaaa	atggcagctt	cagttctaga	5100
gaagaaagaa	caacatcagc	agtaaagtcc	atgggaatagc	tagtggctctg	tgtttctttt	5160
cgccattgcc	tagcttgccg	taatgattct	ataatgccat	catgcagcaa	ttatgagagg	5220
ctaggtcac	caaagagaag	accctatcaa	tgtaggttgc	aaaatctaac	ccctaaggaa	5280
gtgcagtcct	tgatttgatt	tccctagtaa	ccttgagat	atgtttaacc	aagccatagc	5340
ccatgccttt	tgagggtctga	acaaataagg	gacttactga	taatttactt	ttgatcacat	5400
taagggtgtc	tcaccttgaa	atcttataca	ctgaaatggc	cattgattta	ggccactggc	5460
ttagagtact	ccttccccctg	catgacactg	attacaaata	ctttcctatt	catactttcc	5520
aattatgaga	tggactgtgg	gtactgggag	tgatcactaa	caccatagta	atgtctaata	5580
ttcacaggca	gatctgcttg	gggaagctag	ttatgtgaaa	ggcaaataaa	gtcatacagt	5640
agctcaaaaag	gcaaccataa	ttctcttttg	tgcaagtctt	gggagcgtga	tctagattac	5700
actgcacat	tcccaagtta	atcccctgaa	aacttactct	caactggagc	aaatgaactt	5760
tgggtcccaa	tatccatctt	ttcagtagcg	tttaattatgc	tctgtttcca	actgcatttc	5820
ctttccaatt	gaattaaagt	gtggcctcgt	ttttagtcat	ttaaaattgt	tttctaagta	5880
attgtcgcct	ctattatggc	acttcaattt	tgcactgtct	tttgagattc	aagaaaaatt	5940
tctattcatt	tttttgcac	caattgtgcc	tgaactttta	aaatatgtaa	atgctgccat	6000
gttccaaacc	catcgtcagt	gtgtgtgttt	agagctgtgc	accctagaaa	caacatactt	6060
gtcccatgag	cagggtgcctg	agacacagac	ccctttgcat	tcacagagag	gtcattgggt	6120
atagagactt	gaattaataa	gtgacattat	gccagtttct	gttctctcac	aggtgataaa	6180
caatgctttt	tgtgcactac	atactcttca	gtgtagagct	cctgttttat	gggaaaaggc	6240
tcaaatgcc	aattgtgttt	gatggattaa	tatgcccttt	tgccgatgca	tactattact	6300
gatgtgactc	ggttttgcg	cagctttgct	ttgtttaatg	aaacacactt	gtaaacctct	6360
tttgactttt	gaaaaagaat	ccagcgggat	gctcgagcac	ctgtaaacaa	ttttctcaac	6420
ctatttgatg	ttcaaataaa	gaattaaact				6450

<210> 17

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 17

cgctgtaaga tcctgatgaa gtc

23

<210> 18

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 18

tgcctctccc tcgtggtag

19

<210> 19

<211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 19
 tgccttcctt ggatgtggta g

21

<210> 20
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 20
 cgtctgccct atcaactttc g

21

<210> 21
 <211> 920
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 21
 Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser
 1 5 10 15
 Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
 20 25 30
 Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala
 35 40 45
 Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln Gln Gln Gln Gln Gln
 50 55 60
 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 65 70 75 80
 Glu Thr Ser Pro Arg Gln Gln Gln Gln Gln Gly Glu Asp Gly Ser
 85 90 95
 Pro Gln Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu
 100 105 110
 Glu Gln Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys His Pro Glu
 115 120 125
 Arg Gly Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Ser Lys Gly
 130 135 140
 Leu Pro Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser Ala Ala
 145 150 155 160
 Pro Ser Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser
 165 170 175
 Cys Ser Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr Met Gln
 180 185 190
 Leu Leu Gln Gln Gln Gln Gln Glu Ala Val Ser Glu Gly Ser Ser Ser
 195 200 205
 Gly Arg Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser Lys Asp Asn
 210 215 220

Tyr Leu Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys Glu Leu Cys
 225 230 235 240
 Lys Ala Val Ser Val Ser Met Gly Leu Gly Val Glu Ala Leu Glu His
 245 250 255
 Leu Ser Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala Pro Leu
 260 265 270
 Leu Gly Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala Pro Leu Ala
 275 280 285
 Glu Cys Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys Ser Thr Glu
 290 295 300
 Asp Thr Ala Glu Tyr Ser Pro Phe Lys Gly Gly Tyr Thr Lys Gly Leu
 305 310 315 320
 Glu Gly Glu Ser Leu Gly Cys Ser Gly Ser Ala Ala Ala Gly Ser Ser
 325 330 335
 Gly Thr Leu Glu Leu Pro Ser Thr Leu Ser Leu Tyr Lys Ser Gly Ala
 340 345 350
 Leu Asp Glu Ala Ala Ala Tyr Gln Ser Arg Asp Tyr Tyr Asn Phe Pro
 355 360 365
 Leu Ala Leu Ala Gly Pro Pro Pro Pro Pro Pro His Pro His
 370 375 380
 Ala Arg Ile Lys Leu Glu Asn Pro Leu Asp Tyr Gly Ser Ala Trp Ala
 385 390 395 400
 Ala Ala Ala Ala Gln Cys Arg Tyr Gly Asp Leu Ala Ser Leu His Gly
 405 410 415
 Ala Gly Ala Ala Gly Pro Gly Ser Gly Ser Pro Ser Ala Ala Ala Ser
 420 425 430
 Ser Ser Trp His Thr Leu Phe Thr Ala Glu Glu Gly Gln Leu Tyr Gly
 435 440 445
 Pro Cys Gly Gly Gly Gly Gly Gly Gly Gly Glu Ala Gly Ala Val Ala Pro
 450 455 460
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Glu Ala Gly Ala Val Ala Pro
 465 470 475 480
 Tyr Gly Tyr Thr Arg Pro Pro Gln Gly Leu Ala Gly Gln Glu Ser Asp
 485 490 495
 Phe Thr Ala Pro Asp Val Trp Tyr Pro Gly Gly Met Val Ser Arg Val
 500 505 510
 Pro Tyr Pro Ser Pro Thr Cys Val Lys Ser Glu Met Gly Pro Trp Met
 515 520 525
 Asp Ser Tyr Ser Gly Pro Tyr Gly Asp Met Arg Leu Glu Thr Ala Arg
 530 535 540
 Asp His Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys
 545 550 555 560
 Leu Ile Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr
 565 570 575
 Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln
 580 585 590
 Lys Tyr Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe His
 595 600 605
 Arg Lys Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly
 610 615 620
 Met Thr Leu Gly Ala Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu
 625 630 635 640
 Gln Glu Glu Gly Glu Ala Ser Ser Thr Thr Ser Pro Thr Glu Glu Thr
 645 650 655
 Thr Gln Lys Leu Thr Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro
 660 665 670
 Ile Phe Leu Asn Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala
 675 680 685
 Gly His Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser
 690 695 700

Leu Asn Glu Leu Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala
 705 710 715 720
 Lys Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala
 725 730 735
 Val Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp
 740 745 750
 Arg Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp
 755 760 765
 Leu Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln
 770 775 780
 Cys Val Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile
 785 790 795 800
 Thr Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile
 805 810 815
 Ile Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg
 820 825 830
 Met Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys
 835 840 845
 Asn Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu
 850 855 860
 Asp Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp
 865 870 875 880
 Leu Leu Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met
 885 890 895
 Ala Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val
 900 905 910
 Lys Pro Ile Tyr Phe His Thr Gln
 915 920

<210> 22

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 22

Pro Lys Lys Phe Arg Ser Leu Phe Phe Gly Ser Ile
 1 5 10

<210> 23

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 23

His Pro Thr His Ser Ser Arg Leu Trp Glu Leu Leu Met Glu Ala Thr
 1 5 10 15
 Pro Thr Met